

SUBCLASS

FIG. 1

BLASTP - query = 147_TR1; Hit = swiss|O15393|TMS2_HUMAN

This hit is scoring at : 3e-66 (expectation value)
Alignment length (overlap) : 370
Identities : 38 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb

Q: 36 CDGVVDCKLKSDELGCVRFDWDKSLKIYSGSSHQWLPICSSNWNDSEKTCQQLGFES
CDGV .C. .DE CVR. . :L::YS.....W P:C::WN::Y....C::G:::
H: 133 CDGVSHCPGGEDENRCVRLYGPNFILQMYSSQQRKSWHPVCQDDWNENYGRAACRDMGYKN

AHRTTEVAHRDFANSFSILRYNST IQESLHRSE CPSQRYISLQCSHCGLRA
... :D :S S::N:: I::L::S: C.S:::SL:C CG:: :
NFIYSSQGIVDD SGSTSFMKLNTSAGNVDIYKKLYHSDACSSKAVVSLRCLACGVNLNSS

MTGRIVGGALASDSKWPWQVSLHFGTTHXGGTLIDAQWVLTAAHCFVVTREKVLGEG---
...RIVGG. A ...WPWQVSLH. ...H:CGG::I::W::TAAHC. EK L..
RQSRIVGGESALPGAWPWQVSLHVQNVHVCSSIIITPEWYTAHCV EKPLNNPWH

TRYPSIN HIS

WKVYAGTSNLHQLPEAAS--IAEIIINSNYTDEEDDYDIALMRLSKHETLSGEGICTP
W...AG. . . : .A.I :.NY..... DIALM:L.KPLT... : :C.P
WTAFAGILRQSFMYGAGYQVQKVISHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLP

RSPAPQPQHPLQPSHLSASVNSYPGPKASADKTSPFLREVQVNLIDFKKCNDYLVYDSYL
P LQP..L . : : : G.....KTS..L...:V LI: : :CN. .VYD:::
N PGMMLQPEQL-CWISGWGATEEKGKTSEVLNAAKVLLIETQRCNSRYVYDNL

TPRMMCAGDLRGGRDSCQGDSCGGPLVCEQNNRWYLAGVTSWGTGCGQRNKPQVYTKVTEV
TP.M:CAG L:G. DSCQGDSCGGPLV...NN W:L:G TSWG:GC... :PGVY .V..
TPAMICAGFLQGNVDSQGDSCGGPLVTSNNNIWWLIGDTSWGSACAKAYRPGVYGNVMVF

TRYPSIN_SER

LPWIYSKMEA 389
..WIY.:M:A
TDWIYRQMA 490

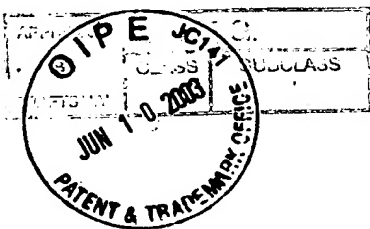


FIG. 2

Prosite search results

PS00134	187->193 TRYPSIN_HIS	PDOC00124
PS00135	334->346 TRYPSIN_SER	PDOC00124

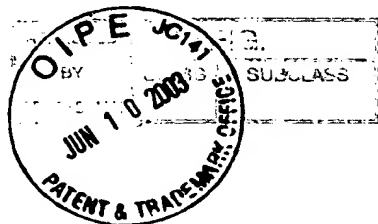


FIG. 3

BLOCKS search results

AC#	Description	Strength	Score
BL00495N AA#	Apple domain proteins. 325 AGdlrGGrDsCqGDSGGPLVCeqNnRWyLaGvTSW (SEQ ID NO:15)	1945	1582
BL01253G AA#	Type I fibronectin domain proteins. 332 rDsCQGDSSGGPLVC (SEQ ID NO:16)	1641	1548
BL00134A AA#	Serine proteases, trypsin family, histidine p 175 CGGTLIDaQWVLTAHC (SEQ ID NO:17)	1500	1524
BL00021D AA#	Kringle domain proteins. 341 GPLVCEQNNRWYLaGVTSWgtGCGQRNKPgVYTKVTevLPWI (SEQ ID NO:18)	1556	1510
BL01253H AA#	Type I fibronectin domain proteins. 351 WYLaGvtSWgtGCGQRNKPgVYTKVTevLpWIysk (SEQ ID NO:19)	1765	1508
BL00021B AA#	Kringle domain proteins. 175 CGGTLIDaQWVLTAHC (SEQ ID NO:20)	1547	1507
BL00495O AA#	Apple domain proteins. 360 GtGCGQRnkPGVYTKVTevlpWIysKmeA (SEQ ID NO:21)	1756	1383
BL00134B AA#	Serine proteases, trypsin family, histidine p 333 DSCQGDSSGGPLVCEqNNRWYLAGV (SEQ ID NO:22)	1289	1299
BL01209 AA#	LDL-receptor class A (LDLRA) domain proteins. 35 CDGVVDCKlKSDE (SEQ ID NO:23)	1413	1274
BL01253F AA#	Type I fibronectin domain proteins. 288 AdktSpFLREvQVnLidfkKCndylVYdSylTPrMmCAG (SEQ ID NO:24)	1693	1270
BL00495L AA#	Apple domain proteins. 209 tSnlhqlpeaaSlaEIIInsNYtdeEddyDIALmrLskP (SEQ ID NO:25)	1947	1263
BL00134C AA#	Serine proteases, trypsin family, histidine p 369 PGVYTKVTEVLPWI (SEQ ID NO:26)	1245	1254
BL01253D AA#	Type I fibronectin domain proteins. 175 CGGtLIdaqWVLTA (SEQ ID NO:27)	1398	1217

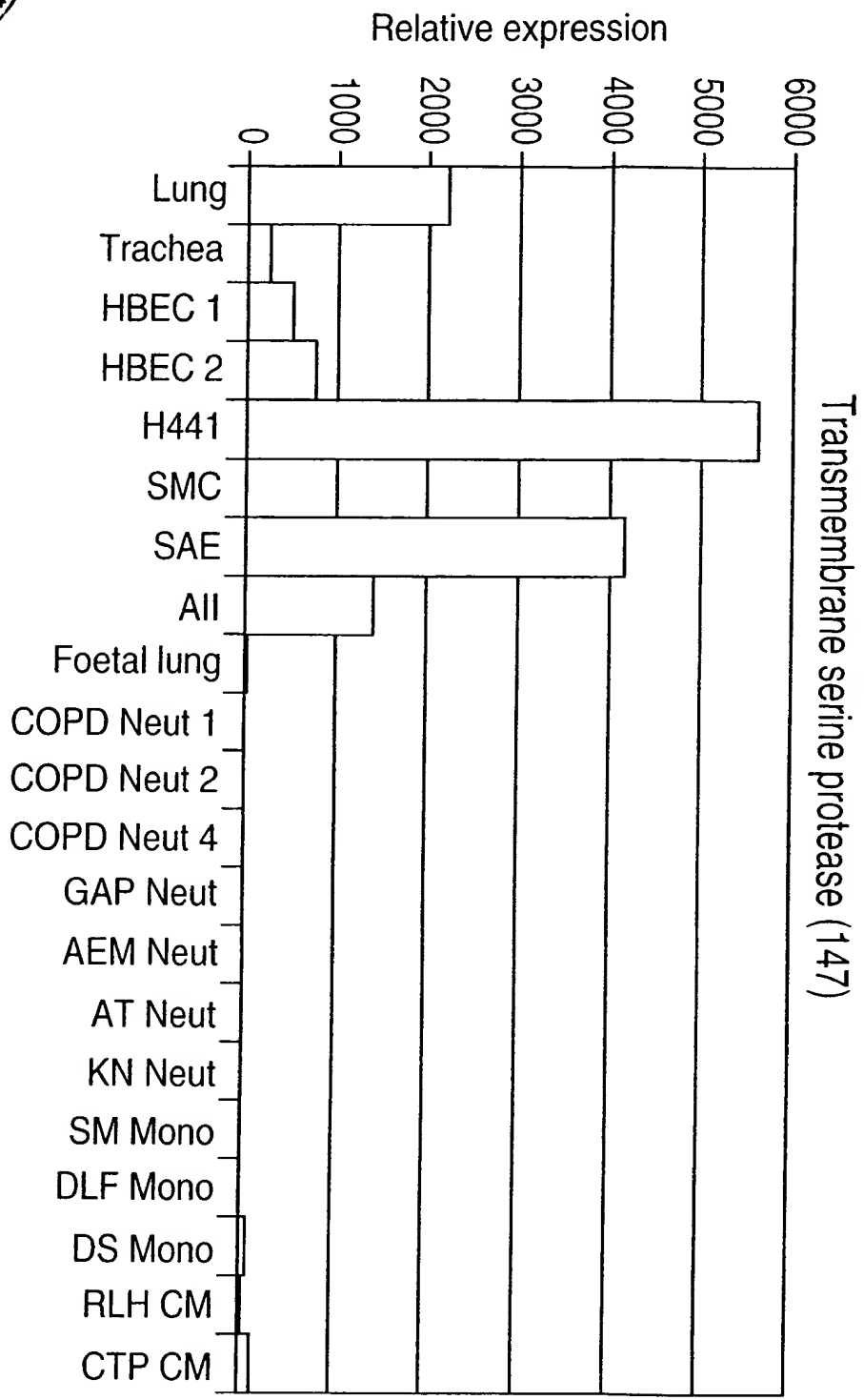


FIG. 4

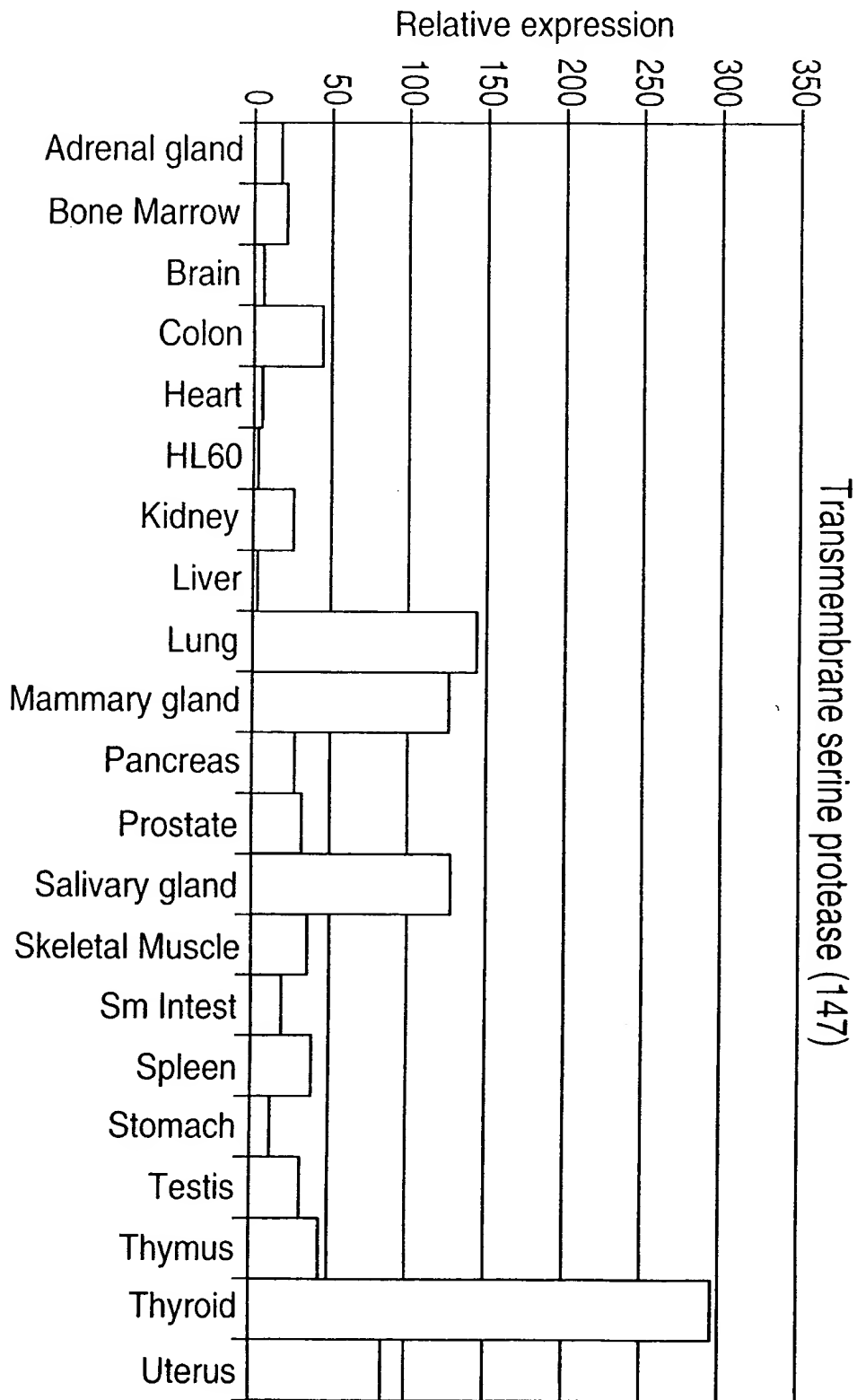
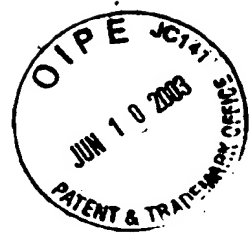
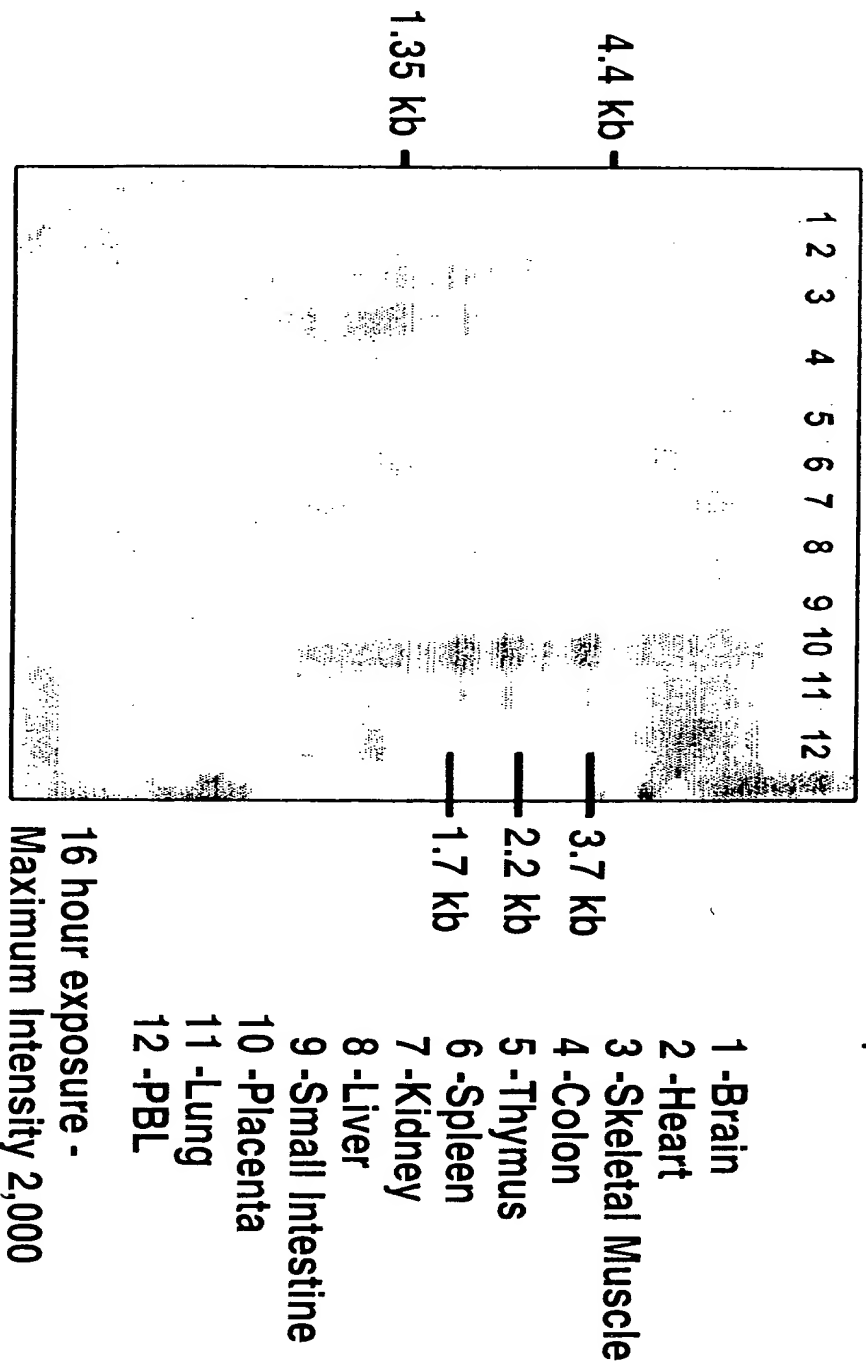


FIG. 5

FIG. 6

LBRI -147 - Transmembrane serine protease



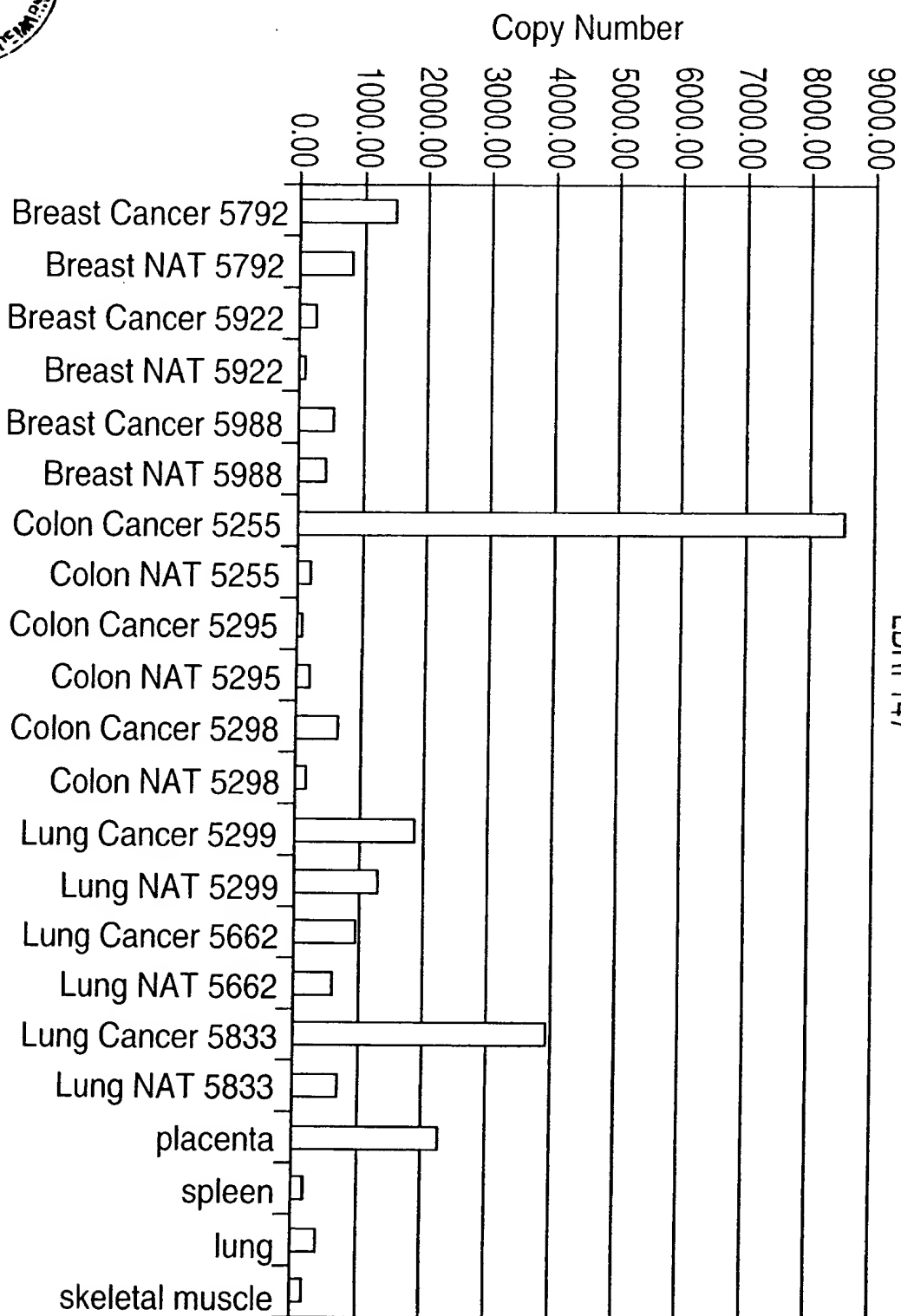


FIG. 7
LBRI 147



FIG. 8
LBRI 147: Fold Change

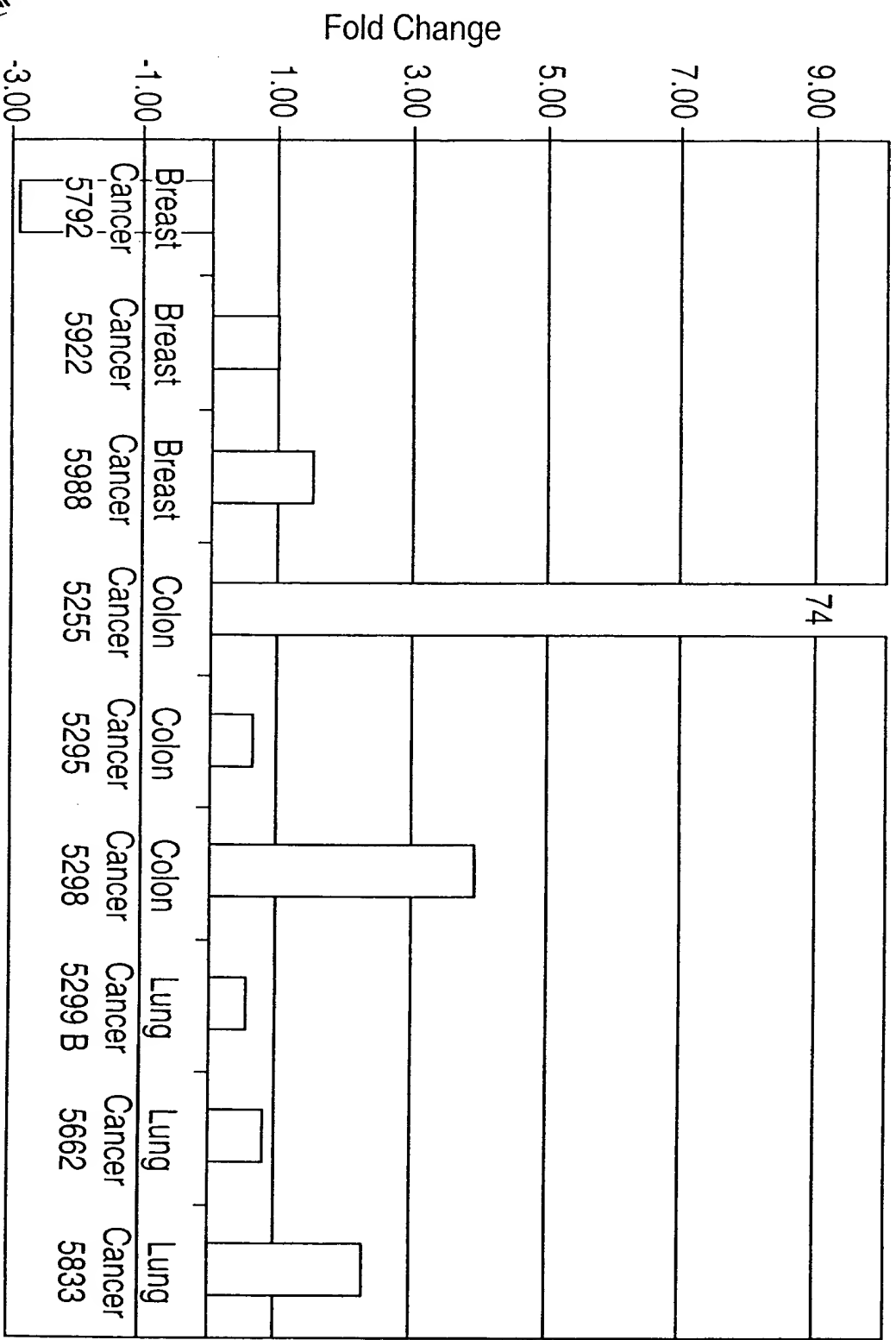


FIG. 9

